<110> Mercola, Daniel
       Adamson, Eileen
       de Belle, Ian

<120> Isolation and Identification of Control Sequences and Genes Modulated by Transcription

<130> ADA.001CIP1

<140> US 10/032,260
<141> 2001-12-20

<150> US 09/270,391
<151> 1999-03-16

<160> 27

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<110> Mercola, Daniel
       Adamson, Eileen
       de Belle, Ian

<120> Isolation and Identification of Control Sequences and Genes
Modulated by Transcription Factors

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Pro Gln Ser His
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gctagtagtc caggttcccg tagtggatgt gcaaagcaac aacttcaagg agatgtggcc
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gtcatgctgc caggacccgt tctatccttt ccctgggcct cgcctgcttc aagcggcagc
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aggagtatgt catagaacca aagtctgtgc agttcctgat acagcatggc ttcaacttca
    480

accagcagta tgcccaaggc atcccctacc ataagggcaa tgacaagggt gatgagagcc
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    600

ctacacaatg gccttataga cttggtgttc ctgtaccaaa acttctatgc acacctccct
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gagagtctgg gaaccttcac cgctgacctg tgtgagatgt tcccagcagg catttatgac
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accaaatatg ctgctgagtt tcatgcccgt ttcgtggcct cctacttaga atatgccttc
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aaaatgggaa gcagcgggca gctggcagcc cacaccttac cctggagttc tgcaactatc
    960

cttccagcat gagggaccat attgattacc gctgctgcct gcccccagca acccaccgtc
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    1080

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    1140

acaagcggcg acggcgacga cgtagggaaa aacggaagag ggctttattg aacctaccgg
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gcatcaagcc tgaagaaacc gagcaggagg tggctgccga tgaaactagg aacctgcctc
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tggaagtgag ccagggaccg caaccctgca gctctggacc ctggctccct gaatgccaca
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ataaggtata tttgagtggc aaagctgtac ccctcacagt ggccaagagc cagttctctc
   1620

gttcctccaa agcccacaat cagaagatga agctcacttg gggcagtagc tgatgcaact
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tccaccttgc tctcaggtgg aacagaggta ttttgggtct ctctagcctg aaatgtcatc
   1740

ctcaactgct actgagtttg ggggagggggg aatgtcttga cagacatcac tgcattgccc
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tggaccgcct cctttatccc agtgtttgag gtacaagtaa gaaggctgac cagcacctgt
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aacactgact ttatttttaa gtctgaaaat gtcttgggaa agttttacaa aaaaaaaaat
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Cys Pro Leu Gly Pro Gln Cys Pro Gln Ser His Asp Ile Asp Pro Ile
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Ile Asp Thr Asp Glu Ala Ala Ala Glu Asp Lys Arg Arg Arg Arg Arg
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Arg Arg Glu Lys Arg Lys Arg Ala Leu Leu Asn Leu Pro Gly Thr Gln
65                  70              75                  80

Thr Ser Gly Glu Ala Lys Asp Gly Pro Pro Lys Lys Gln Val Cys Gly
            85              90                  95

Asp Ser Ile Lys Pro Glu Glu Thr Glu Gln Glu Val Ala Ala Asp Glu
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Thr Arg Asn Leu Pro His Ser Lys Gln Gly Asn Lys Asn Asp Leu Glu
        115             120             125

Met Gly Ile Lys Ala Ala Arg Pro Glu Ile Ala Asp Arg Ala Thr Ser
    130             135             140

Glu Val Pro Gly Ser Gln Ala Ser Pro Asn Pro Val Pro Gly Gly Gly
145             150             155             160

Leu His Arg Ala Gly Phe Asp Ala Phe Met Thr Gly Tyr Val Met Ala
            165             170             175

Tyr Val Glu Val Ser Gln Gly Pro Gln Pro Cys Ser Ser Gly Pro Trp
            180             185             190
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Leu Pro Glu Cys His Asn Lys Val Tyr Leu Ser Gly Lys Ala Val Pro
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cccacctttc cccctttttct attccacaaa accgccattg tcatcatggg ccgttctcaa
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tgagctgttg ggtgagatat tagaattcta ctcacagaac gaaatgaaaa gtctcccatg
    240

tctacttctt ctacacaaga cacagcaaca tccgatttct caatcctttc cccaactttc
    300

cccctttttct antccacaan accgccattg tcatcatggg ncgttctcaa tgagctgttg
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ggtgagatat tagaattctg ggctgggaat gagttcagcc tggtggaatg tgaacctgca
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ncagtttggc atgaacgggc aaatgctgtg tancctccgg aaaggagcgc ttcctggaag
    480
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ctggcgcctg actttgtggg ngacatcctc cgggaaaang gttcactant tctaaagcgg
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gcggcaacgc ggtggggctc caattcgccc taaantgngt ccgtattaca attcacnggg
    600

cggccgtttt anaagtcctg nncggggaaa accnggggta nccaacttta tcnccctggn
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ngaaancccc ccttncncaa cngggtnan aaccnannng ggccncccnn tttgcccctc
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ccaa
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    120

tgaagagatt aacatgggaa tgtcataata attgaatcta aagaagacat aatttcaaaa
    180

taagagcttg agtaataata ccattgtgta acaatctgat ttccatccct cttatttttc
    240

ctatattatg cagtttagtt ctttactatc atgtgtttca tgtttgttcg gttttaccaa
    300
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cacatcatta gtaaattgaa tgtaaggctt ctcatttctt ttgtatccta catctaaaag
    360

attttagtcc ttagaatcct cttgaaatgt tctccattta aaatggagaa atagttcatg
    420

ctctctcatc taagtangag ctaaaatcta aaaaattaat aaataaaata gtccatcctc
    480

taataataat aatgaatact gaanttgtta antaataatt aatttttgag aagggggttc
    540

actaatgcgt ccaagctgga gtgcaatggc gtgatcacta anttctaaan cggcgccaac
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gcggtggagc tccaantn
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    120

ggggaaaggt ggggaaatga ttgagaaatc ggatggttgc tgtgtctgtg tagaaagaag
    180

tagacatggg agacttttca ttttgttctg tgagtagaat tctgggctgg gaatgagttc
    240
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agcctggtga atgtgaacct gcaccagttt ggcatgaacg gncagatgct gtgtaacctc
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ggcaaggagc gcttcctgga gctggcgcct gactttgtgg gcgacatcct ctggnacagg
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ntccactagt tctagagcgg gcgccaccgc ggtggngctc caattcgccc tanagtgngt
   420

cgtnttacaa ttcactggcc gtcgttttac aacgtcgtga ctgggaaaac cctggngtta
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cccaacttaa tcgccttgca gcanatcccc ctttcgncag ctggngtnnt ancgangagg
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nccgcaccgn ttgcccntcc caanaagttg cgcagcctgn atggggantg ggancgncct
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gtnncgggng cantaagcgc ggngggtgtg gtggntangc ncancgtgnn cgnnnnannt
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   120

tgaagagatt aacatgggaa tgtcataata attgaatcta aagaagacat aatttcaaaa
   180

taagagcttg agtaataata ccattgtgta acaatctgat ttccatccct cttattttc
   240
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ctatattatg cagtttaagt tctttactat catgtgtttc atgtttgttc ggttttacca
    300

acacatcatt agtaaattga atgtanggct tctcatttct tttgtatcct acatctaaaa
    360

gattttagtc tttagaatcc tcttgaaatg ttctccattt aaaatggaga aatagttcat
    420

gctctctcat ctaantanga gctaaaatct aaaaaataaa taaataaaat antccatcct
    480

ctaataataa taatgaatac tgaanttgta aataataatt aatttttgag aatggggttc
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    120

agtcagtaag ggagatggat ttgagataca tctcccaact ccttggcagc agcacctggt
    180

taaagcctcc tttcctggca atactatagt ctcagtgatt ggctttcttt gtggtgagca
    240

gcaggaccta gactgaaatt gtagtatttt ggtaacagta tctgctctcc attcaaatct
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    420
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agtgcctttc ctaccatttt acatttggca gactggaaca gctcaaatag ctccaagaaa
    780
gaaaaaactg cctcctttgt ctattcaagg ctctcacttc accttaaatg cagaattttt
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    120
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    180

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    240

ttctcaaggt acaactttga tgcagttcan gtcaaactta ngtaagattt tgttgtanag
    300

tttgggaaat aaccattgtg gcaaggctgg aatgcaaatc gattttttgc tgttacagaa
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ccattcgttt gcattcgata attccattcg attccattgg aggataattc catttgagtc
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cattcgatga ttgttccatt cgattctatt cggtgattcc attcgattcc atttgataat
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gattccaatc gagaccattc gatgattcca ttcaattcca ttcaatcatg atccctttcg
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atccattcga ttccattcta tgacgattcc attcatttca tctgatgatg attccattcg
    420

attcattcag tgataccatt cgattcattc gatgatgatt caatcaattt aatcgatgat
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   120

ttcattgaac ccaatatatg caaaatacta tcatttcaat tataaccaaa ttaaaattaa
   180

ggagatattt tacaattttc atattaacgt ttccaattct ggtgtgaatt ttacactcac
   240

cgaacatctc aattctgaca agtcatattt taagtgctca acagctacgt gaggatagtg
   300

gctattatgt cacaaaatgc agctctangg atgaggacag tttacagaag atacttgagg
   360

atacaggagc aagttaaatg gcagtttaag aaagcaaatc cangatgtgg gaaactccac
   420

agaatanatg acctggtttc tcccttcact catccctcca aaatagaaat caatggcaga
   480

aagaaaaaag anggaggctg ttgtancata aaatacttag ggacatacaa taaaaacagt
   540

gtagggtttt gttgaanccg attcactaca atgattcaca antt
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   120

tgccctgcga aagctctctc ttacctgccg ccatgtaaga ccggactttg ctcctcatta
   180

ggtcaccta gccatgtgga actgtgagtc cattaaacct ctttccttta taaattatgc
   240

agtctcggat atgtctttat tagcaaggtg aaaatgaact aatacaaggg tcacgtggta
   300

aatatattta atattaaaaa aaaatcttcc aaactatttt ccagagtgtc tgtacctttt
   360

tacatttcca tgagcaacgt atgagtgatt tagtttcttt gacagcattt ggtatagtta
   420

ctatttttta ttttagttgt tctcatcctg gacttaattt gaattttccc aatgatgagt
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gatgttgaaa attttcttgt gcttacttgt catctggata ttctcgtcaa taaaatgtct
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cttantatcn tttgcccatt ttcaantgga ttccttttgt gttttatcat tgaattttaa
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gaattcttcn atttatagat atgaattaca gatanaatca tagatattat agatanatat
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gagttatggt tcacnatt
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            35   40   45

Pro Ser Leu Leu Ala Ile Lys Thr Ala Asn Phe Val Ala Val Asp Thr
        50   55   60

Glu Leu Ser Gly Leu Gly Asp Arg Lys Ser Leu Leu Asn Gln Cys Ile
65   70   75   80

Glu Glu Arg Tyr Lys Ala Val Cys His Ala Ala Arg Thr Arg Ser Ile
                85   90   95

Leu Ser Leu Gly Leu Ala Cys Phe Lys Arg Gln Pro Asp Lys Gly Glu
            100   105   110

His Ser Tyr Leu Ala Gln Val Phe Asn Leu Thr Leu Leu Cys Met Glu
        115   120   125

Glu Tyr Val Ile Glu Pro Lys Ser Val Gln Phe Leu Ile Gln His Gly
    130   135   140

Phe Asn Phe Asn Gln Gln Tyr Ala Gln Gly Ile Pro Tyr His Lys Gly
145   150   155   160

Asn Asp Lys Gly Asp Glu Ser Gln Ser Gln Ser Val Arg Thr Leu Phe
            165   170   175

Leu Glu Leu Ile Arg Ala Arg Arg Pro Leu Val Leu His Asn Gly Leu
            180   185   190

Ile Asp Leu Val Phe Leu Tyr Gln Asn Phe Tyr Ala His Leu Pro Glu
            195   200   205

Ser Leu Gly Thr Phe Thr Ala Asp Leu Cys Glu Met Phe Pro Ala Gly
        210   215   220

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225   230   235   240

Ser Tyr Leu Glu Tyr Ala Phe Arg Lys Cys Glu Arg Glu Asn Gly Lys
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Gln Arg Ala Ala Gly Ser Pro His Leu Thr Leu Glu Phe Cys Asn Tyr
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Pro Ser Ser Met Arg Asp His Ile Asp Tyr Arg Cys Cys Leu Pro Pro
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Ala Thr His Arg Pro His Pro Thr Ser Ile Cys Asp Asn Phe Ser Ala
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Tyr Gly Trp Cys Pro Leu Gly Pro Gln Cys Pro Gln Ser His Asp Ile
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Asp Leu Ile Ile Asp Thr Asp Glu Ala Ala Ala Glu Asp Lys Arg Arg
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Arg Arg Arg Arg Arg Glu Lys Arg Lys Arg Ala Leu Leu Asn Leu Pro
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Val Cys Gly Asp Ser Ile Lys Pro Glu Glu Thr Glu Gln Glu Val Ala
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Ala Asp Glu Thr Arg Asn Leu Pro His Ser Lys Gln Gly Asn Lys Asn
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Asp Leu Glu Met Gly Ile Lys Ala Ala Arg Pro Glu Ile Ala Asp Arg
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Ala Thr Ser Glu Val Pro Gly Ser Gln Ala Ser Pro Asn Pro Val Pro
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Gly Pro Trp Leu Pro Glu Cys His Asn Lys Val Tyr Leu Ser Gly Lys
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